

Karaolis1.ST25.1A3
SEQUENCE LISTING

1AP20 Rec'd PCT/PTO 23 JAN 2006

<110> KARAOLIS, David K.R.

<120> METHOD FOR ATTENUATING VIRULENCE OF MICROBIAL PATHOGENS AND FOR INHIBITING MICROBIAL BIOFILM FORMATION

<130> KARAOLIS1 PCT

<140> NOT YET ASSIGNED

<141> 2004-07-22

<150> 60/490,029

<151> 2003-07-25

<160> 5

<170> PatentIn version 3.2

<210> 1

<211> 2055

<212> DNA

<213> V. cholerae

<220>

<221> CDS

<222> (1)..(2055)

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acg tca cac agt ccg ttc ttt ttt gca atc ctc aat gat caa cac caa	96
Thr Ser His Ser Pro Phe Phe Phe Ala Ile Leu Asn Asp Gln His Gln	
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tac gtg atg gtc aac gag cgc tat tgt gat atc gcc ggt ctc tct agc	144
Tyr Val Met Val Asn Glu Arg Tyr Cys Asp Ile Ala Gly Leu Ser Ser	
35 40 45	
gaa gag atg gtc ggg atg agc gat agt cag gtt ctg ggc gaa cat ttt	192
Glu Glu Met Val Gly Met Ser Asp Ser Gln Val Leu Gly Glu His Phe	
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tat cgc cat ctc aaa ccg ttt tac gaa cgt gcg ttt aac aac gag cat	240
Tyr Arg His Leu Lys Pro Phe Tyr Glu Arg Ala Phe Asn Asn Glu His	
65 70 75 80	
att gag tcc gag ctg acc ctc agc gaa atc gac ctc gaa acc agc tta	288
Ile Glu Ser Glu Leu Thr Leu Ser Glu Ile Asp Leu Glu Thr Ser Leu	
85 90 95	
cac ttt tct ctc tcc ccc atc atg atc aac gat cgg gtg caa tac ctt	336
His Phe Ser Leu Ser Pro Ile Met Ile Asn Asp Arg Val Gln Tyr Leu	
100 105 110	
gta ttc cac gcg att gat acc tca gaa aag cag att tta gtg cgc tct	384
Val Phe His Ala Ile Asp Thr Ser Glu Lys Gln Ile Leu Val Arg Ser	
115 120 125	
ctg gaa gaa tcg gaa agc aaa tac gca ctc ctc acg aca ctg cta cct	432
Leu Glu Glu Ser Glu Ser Lys Tyr Ala Leu Leu Thr Thr Leu Leu Pro	
130 135 140	
gat ggt tta atg atg gtg gaa aat gac tgc att att tct gcc aac cct	480
Asp Gly Leu Met Met Val Glu Asn Asp Cys Ile Ile Ser Ala Asn Pro	

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tca tcg cag ttg gct tcg cta ctg aca gaa aaa ccc ttg gtg tgc ttg Ser Ser Gln Leu Ala Ser Leu Leu Thr Glu Lys Pro Leu Val Cys Leu	195	200	205	624
acc ggg cca agg tgt ggg ttt gaa cgg aaa atc cag tta cac gca ggt Thr Gly Pro Arg Cys Gly Phe Glu Arg Lys Ile Gln Leu His Ala Gly	210	215	220	672
tgc acc tct tta ctc ggt aat cag tcg cag ttg atc tta ttg caa gat Cys Thr Ser Leu Leu Gly Asn Gln Ser Gln Leu Ile Leu Leu Gln Asp	225	230	235	720
gcc gat gaa gcc cca aaa cag ttt tct gcg acc act caa gtc gat gcg Ala Asp Glu Ala Pro Lys Gln Phe Ser Ala Thr Thr Gln Val Asp Ala	245	250	255	768
cat att gat agc ctc act ggg ctg tat aac cga cac ggg ttt acc aag His Ile Asp Ser Leu Thr Gly Leu Tyr Asn Arg His Gly Phe Thr Lys	260	265	270	816
cgc tta gag cag tgc atc caa aat gag acg cct ttg gtt atg ctc tat Arg Leu Glu Gln Cys Ile Gln Asn Glu Thr Pro Leu Val Met Leu Tyr	275	280	285	864
ctg gac att gat aac ttc aaa aac atc aat gac tct ctc ggc cat cac Leu Asp Ile Asp Asn Phe Lys Asn Ile Asn Asp Ser Leu Gly His His	290	295	300	912
atc ggt gac aaa gtg att aaa gag gtg gcg gca cgt tta aaa cgc tta Ile Gly Asp Lys Val Ile Lys Glu Val Ala Ala Arg Leu Lys Arg Leu	305	310	315	960
ctg cca cag caa gcc gta ctt ggc cat ttg ggc ggt gat gag ttt ggt Leu Pro Gln Gln Ala Val Leu Gly His Leu Gly Gly Asp Glu Phe Gly	325	330	335	1008
ttg atc ttg ccg gag cca gaa cac aac cgc tct gca gaa atg ttg gca Leu Ile Leu Pro Glu Pro Glu His Asn Arg Ser Ala Glu Met Leu Ala	340	345	350	1056
gat cgc att atc tct ttg att aat cag cct ttt gac ctg cac cat ttc Asp Arg Ile Ile Ser Leu Ile Asn Gln Pro Phe Asp Leu His His Phe	355	360	365	1104
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ggc aat gat gct cgc gta tta ctg caa aat gcc gat acc gcg atg tat Gly Asn Asp Ala Arg Val Leu Leu Gln Asn Ala Asp Thr Ala Met Tyr	385	390	395	1200
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Ala	Glu	Lys	Ala	Gly	Leu	Ile	Glu	His	Leu	Gly	Arg	Val	Val	Met	Arg					
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Glu	Val	Phe	Ala	Thr	Val	Lys	Arg	Trp	Lys	Leu	Gln	Gly	Ile	Leu	Pro					
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Gly	Arg	Val	Ala	Ile	Asn	Ile	Ser	Pro	Glu	Gln	Phe	Gly	Asn	Pro	Gln					
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aac	aac	atc	aca	ttt	gaa	ctg	acc	gaa	agt	gtg	gtg	atg	agc	gat	agt	1680				
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act	cag	caa	caa	gcc	act	tta	ctc	tcc	aac	cta	aat	tgc	cac	tcc	atc	1968				
Thr	Gln	Gln	Gln	Ala	Thr	Leu	Leu	Ser	Asn	Leu	Asn	Cys	His	Ser	Ile					
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caa	ggc	ttc	cat	ttt	tat	cgc	cca	caa	ccg	aag	cac	gaa	gtg	gaa	gag	2016				
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<211> 684

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<213> V. cholerae

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Tyr Val Met Val Asn Glu Arg Tyr Cys Asp Ile Ala Gly Leu Ser Ser
 35 40 45

Glu Glu Met Val Gly Met Ser Asp Ser Gln Val Leu Gly Glu His Phe
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Tyr Arg His Leu Lys Pro Phe Tyr Glu Arg Ala Phe Asn Asn Glu His
 65 70 75 80

Ile Glu Ser Glu Leu Thr Leu Ser Glu Ile Asp Leu Glu Thr Ser Leu
 85 90 95

His Phe Ser Leu Ser Pro Ile Met Ile Asn Asp Arg Val Gln Tyr Leu
 100 105 110

Val Phe His Ala Ile Asp Thr Ser Glu Lys Gln Ile Leu Val Arg Ser
 115 120 125

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 130 135 140

Asp Gly Leu Met Met Val Glu Asn Asp Cys Ile Ile Ser Ala Asn Pro
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Glu Asn Leu Ser Arg Leu Phe Ile Asp Glu Lys Thr Lys Thr Val Phe
 180 185 190

Ser Ser Gln Leu Ala Ser Leu Leu Thr Glu Lys Pro Leu Val Cys Leu
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Thr Gly Pro Arg Cys Gly Phe Glu Arg Lys Ile Gln Leu His Ala Gly
 210 215 220

Cys Thr Ser Leu Leu Gly Asn Gln Ser Gln Leu Ile Leu Leu Gln Asp
 225 230 235 240

Ala Asp Glu Ala Pro Lys Gln Phe Ser Ala Thr Thr Gln Val Asp Ala
 245 250 255

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His Ile Asp Ser Leu Thr Gly Leu Tyr Asn Arg His Gly Phe Thr Lys
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 Arg Leu Glu Gln Cys Ile Gln Asn Glu Thr Pro Leu Val Met Leu Tyr
 275 280 285
 Leu Asp Ile Asp Asn Phe Lys Asn Ile Asn Asp Ser Leu Gly His His
 290 295 300
 Ile Gly Asp Lys Val Ile Lys Glu Val Ala Ala Arg Leu Lys Arg Leu
 305 310 315 320
 Leu Pro Gln Gln Ala Val Leu Gly His Leu Gly Gly Asp Glu Phe Gly
 325 330 335
 Leu Ile Leu Pro Glu Pro Glu His Asn Arg Ser Ala Glu Met Leu Ala
 340 345 350
 Asp Arg Ile Ile Ser Leu Ile Asn Gln Pro Phe Asp Leu His His Phe
 355 360 365
 Ser Lys Arg Leu Ala Cys Ser Ile Gly Ser Val Arg Tyr Pro Gly Asp
 370 375 380
 Gly Asn Asp Ala Arg Val Leu Leu Gln Asn Ala Asp Thr Ala Met Tyr
 385 390 395 400
 Glu Ala Lys Glu Arg Gly Arg Asn Arg Leu Ile Lys Phe Asn Asp Gln
 405 410 415
 Met Asn Lys Glu Ala Arg Met Arg Leu Trp Leu Glu Ile Glu Leu Gln
 420 425 430
 Lys Ala Leu Gln Gln Asn Gly Leu Glu Val Trp Tyr Gln Pro Lys Val
 435 440 445
 Asn Ala Arg Asp Phe Ser Ile Asn Gly Ala Glu Ala Leu Val Arg Trp
 450 455 460
 Lys His Pro Val Glu Gly Tyr Ile Ser Pro Gly Ala Phe Ile Pro Val
 465 470 475 480
 Ala Glu Lys Ala Gly Leu Ile Glu His Leu Gly Arg Val Val Met Arg
 485 490 495
 Glu Val Phe Ala Thr Val Lys Arg Trp Lys Leu Gln Gly Ile Leu Pro
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 Gly Arg Val Ala Ile Asn Ile Ser Pro Glu Gln Phe Gly Asn Pro Gln
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Leu Ile Asp Tyr Leu Glu Lys Leu Leu Arg Thr Thr Gly Leu Asp Pro
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 580 585 590

Ala Arg Phe Pro Ile Asp Glu Leu Lys Ile Asp Arg Ala Phe Ile Ser
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Asn Ile Asp Thr Leu Pro Lys Gln Leu Thr Val Ile Glu Asn Ile Ile
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Thr Gln Gln Gln Ala Thr Leu Leu Ser Asn Leu Asn Cys His Ser Ile
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<222> (3)..(3)

<223> Residue at this position can be either Asp or Glu.

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